

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 9, 2002, 16:22:02 ; Search time 1762.53 Seconds
(without alignments)
2389.208 Million cell updates/sec

Title: US-09-880-887-9

Sequence: 1 gttgtttatgcacccctttt.....cgtatcttttaccattcag 312

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estcov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	47.2	15.1	734	12	CNS010MP
C 2	46.8	15.0	1101	12	CNS0039G
C 3	46.8	15.0	1101	12	CNS016L1
C 4	42.8	13.7	827	12	CNS00EUD
5	42.6	13.7	1225	12	CNS0161D
6	42.4	13.6	948	12	CNS0159T
7	42	13.5	637	12	CNS036C
8	41.6	13.3	1101	12	CNS00H87
C 9	41	13.1	402	12	CNS00H87
C 10	41	13.1	979	12	BT314726
C 11	40.8	13.1	810	12	CNS0161W
C 12	40.8	13.1	940	12	CNS010Y8
C 13	40.6	13.0	483	9	BB247254
C 14	40.6	13.0	987	12	CNS014PO
C 15	40.4	12.9	524	12	CNS01U90
C 16	40.2	12.9	555	10	BT977182
C 17	40.2	12.9	987	12	CNS014PO

C 18	40	12.8	887	12	CNS00D5M	AL060256 Drosophila
C 19	40	12.8	1004	12	CNS00B2	AL058076 Drosophila
C 20	40	12.8	1101	12	CNS00962	AL097301 Drosophila
C 21	39.8	12.8	817	12	A2689592	A2689592 ENTHA57TR
C 22	39.8	12.8	856	12	A2680208	A2680208 ENTHA57TR
C 23	39.8	12.8	874	12	BT135257	BT135257 ENTHA57TR
C 24	39.8	12.8	896	12	CNS020G5	AL1214430 Tetradodon
C 25	39.8	12.8	1101	12	CNS016TX	AL107199 Drosophila
C 26	39.6	12.7	495	12	AO192980	AO192980 HS_3053_A
C 27	39.4	12.6	915	12	CNS048RF	AL1779636 Tetradodon
C 28	39.4	12.6	945	12	CNS04DOK	AL285149 Tetradodon
C 29	39.2	12.6	469	10	BM213762	BM213762 C0841C11-
C 30	39.2	12.6	675	12	A2974879	A2974879 C0841C11-
C 31	39.2	12.6	758	10	BS214880	BS214880 RST34535
C 32	39.2	12.6	1101	12	CNS00EFA	AL069119 Drosophila
C 33	39.2	12.6	1201	12	CNS0167M	AL106396 Drosophila
C 34	38.8	12.4	445	10	BE96412	BE96412 QV0-CT038
C 35	38.8	12.4	543	10	BM214243	BM214243 C0847H03-
C 36	38.8	12.4	548	10	BM216550	BM216550 C0882D04-
C 37	38.8	12.4	550	10	BM212068	BM212068 C0816F07-
C 38	38.8	12.4	578	10	BM214914	BM214914 C0857G10-
C 39	38.8	12.4	581	10	BM214098	BM214098 C0846B01-
C 40	38.8	12.4	646	10	BM213857	BM213857 C0842E11-
C 41	38.8	12.4	669	10	BM212059	BM212059 C0816E10-
C 42	38.8	12.4	683	9	AL514415	AL514415
C 43	38.8	12.4	898	12	A2543560	A2543560 ENTDP60TR
C 44	38.6	12.4	695	12	AG043691	AG043691 Pan trogl
C 45	38.6	12.4	948	12	CNS0159T	AL105179 Drosophila

ALIGNMENTS

RESULT 1
CNS010MP/c
LOCUS
DEFINITION
CNS010MP
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN04L20 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION
AL099163
VERSION
AL099163.1 GI:5610774
KEYWORDS
GSS.
SOURCE
fruit fly.
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 734)
Genoscope.
AUTHORS
Direct Submission
TITLE
Submitted (23-JUL-1999) Genoscope - Centre National de Recherche
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
JOURNAL

COMMENT
- Web : www.genoscope.cns.fr
- Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EGP) -
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billand at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos from Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
peloBAC11.

FEATURES
source
1..734
Location/Qualifiers
/organism="Drosophila melanogaster"
/plasmid="peloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN04L20"
/note="end : T7"

BASE COUNT
ORIGIN
288 a 62 c 2 g 211 t 171 others

	Query Match	15.1%	Score 47.2:	DB 12;	Length 734:	
	Best Local Similarity	33.2%:	Pred. No.1.9:	Mismatches 149;	Indels 0;	Gaps 0:
	Matches 103:	Conservative 58;	NonMatches 149;	Indels 0;	Gaps 0:	
OY	2 ttgttgatgcaccccttttaataacatagatgcttgccttttagatatagaat 61					
	: :	:	:	:	:	:
Db	350 TTATATTWTTTWTATTTTWTTTTMMTKATATTTTGTAFTWTTTDDCKMMAAATTAAT 291					
OY	62 atcgtatgctgctcttcactcaaatlittgatatacatgattggacaagcattaaagg 121					
	: :	:	:	:	:	:
Db	290 ATWGWTTTTKATTTTTTGTGTTWWTKTATAMWWWMTKTITTTKMWAATFTWTWT 231					
OY	122 tctaaccagccagcacagcgagtgtgaagfagctgtggacaacacacagatttggctccat 181					
	: :	: :	: :	: :	: :	: :
Db	230 KTTAAAWTAATAATATWTTWTWTWTWTTWTKAKMTWTATWAMAANAATWTRAKKMWTTT 171					
OY	182 gccctcaagaagaaatgaccttcagatcatcttggattaacaaaagacttccttaagag 241					
	: :	:	:	:	:	:
Db	170 AAAAAATTTTTTAATKAANAAAAATATWTKAAAANKAAAAATWATAATATWTKDWTAWWT 111					
OY	242 atgtaaatttcacgatgttctcttttggtaaacaacaaagaattaacgtaattctt 301					
	: :	: :	: :	: :	: :	: :
Db	110 TTTWTTTTHHKKAAATTTCAAMKRTTTTWTWTWATWTATATATATATATATATATKTWT 51					
OY	302 ttacattcca 311					
	: :	:	:	:	:	:
Db	50 TTTTATATGA 41					
RESULT 2	CNS00396	1101 bp	DNA	GSS 03-JUN-1999		
LOCUS	CNS00396/c					
DEFINITION	Drosophila melanogaster genome survey sequence TE13 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.					
ACCESSION	AL063921					
VERSION	AL063921.1	GI:4941778				
KEYWORDS	GSS.					
SOURCE	fruit fly.					
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 1101)					
REFERENCE	Genoscope.					
AUTHORS	Direct Submission					
TITLE	Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :					
JOURNAL	BP 191 J1006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazuo Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.					
COMMENT						
FEATURES	Source					
	Location/Qualifiers					
	1..1101					
	/organism="Drosophila melanogaster"					
	/db_xref="taxon:7227"					
	/clone_lib="RPCI-98"					
	/clone="BACR08K10"					
	/note="end : FE13"					
BASE COUNT	201 a 64 c 131 g 202 t 503 others					
ORIGIN						

Query Match	Similarity	Score	DB 12	Length	1101
Best Local	Similarity	25.9%	Pred. No. 2.2	113	Indels
Matches	76	Conservative	103	Mismatches	113
					Indels
					Gaps
					1

Db 790 TTTTWTAAATATTWTTWTTDTATTTTTTTTTTWAMTAATATTTTWAMTAATAATTAMAATW 849

Oy 62 atctgaagcgcgtctcttctaactaaatttgtaatacatgattggacaagaacatctgaag 121
Db 850 WTATTAAATATAMMATATMTWMMWWMTRTAAMWMDWTWMMWTTAKTTWAATATAATMTAW 909

Oy 122 tctaacaccgcacgcacggttgtgaagtactcgtagaacatcaagaatttgccat 181
Db 910 AAMTAAAMMAAAATATATWTTWTTAATTADMTKTTASTATWTTTDITWTTAARAKARMAT 969

Oy 182 gccctaaagaagaattgcttcagattatcttgtaataaaaagaaccttctaag 241
Db 970 WDMAAMAMTATAMDRTATWATATADATATWATAAAMWTTWMDTATTGWRMWTADATAMDA 1029

Oy 242 atgtaaaattccaagatgattctttcttgtaaactaaagaataacgcgatctt 301
Db 1030 ATRTAAATWTTTKMTTKMTTKMTTKTKAKTKAKARAWMMWMTKAARRRMRRTCAD 1089

Oy 302 ttacattcca 311
Db 1090 ATATATATAA 1099

RESULT	4
CNS00EJ/c	
LOCUS	827 bp DNA linear GSS 04-JUN-1999
DEFINITION	Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL069854
VERSION	AL069854.1 GI:4949806
KEYWORDS	GSS.
SOURCE	fruit fly.
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 827)
REFERENCE	Genoscope. Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammosser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by Buffalo, ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm .
FEATURES	Location/Qualifiers 1..827 /organism="Drosophila melanogaster" /db_xref="taxon:7227" clone_lib="RPCI-98" /clone="BACR29B23" /note="end : TET3"
BASE COUNT	181 a 107 c 46 g 163 t 330 others
ORIGIN	
Query Match	13.7%; Score 42.8; DB 12; Length 827;
Best Local Similarity	20.2%; Pred. No. 16;
Matches	55; Conservative 109; Mismatches 108; Indels 0; Gaps 0;

Qy	39	gcttgcscctttaagatataagaatcttgatctgctctctcgaacaaatttgattgaat	98
Db	790	GMKMBYDKAKMTKMRMDAAKGHRHGGRRKKWGKTKTKTNRHKKKWGSTAYSAVAVT	731
Qy	99	gatttgacaagaataattgaagagcttlaacagacagacgcagattggtgaagtactgtgg	158
Db	730	AAVTGMHNHWMATDADATGAMMMMMWMTATRKVKRRKRDADDTRGDMKTRCKDTAKTSAG	671
Qy	159	aaacacacagatttgctgcscatgcscctaaagagaatctgctcttcagatatttgact	218
Db	670	AGDYVABAATATWTTTNNWTTTWNHNTTKTKWNTHTAAAMRRKADADADAAMWMTWRW	611
Qy	219	aaaaacaagaactctctaaagatgataaattctacgatcttctctttcttgaataa	278
Db	610	NRATYAMWTTDATTMDADALNHNHAKKATWMDAHNMWMTAAMKMKYVWMDYTTWNSKYSBW	551
Qy	279	ctaaagaattaacgcgcgtactctcttcaacttc	310
Db	550	HNHCSTANATAMAGNDTADHNWTTTMAAHTNW	519

LOCUS	CSN0161D	1225 bp	DNA	linear	GSS 26-JUL-1999
DEFINITION	Drosophila melanogaster genome survey sequence Sfe end of BAC				
ACCESSION	BA0161C18 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.				
VERSION	AL106171				
KEYWORDS	GSS.				
SOURCE	AL106171.1 GI:5620504				
ORGANISM	fruit fly.				
REFERENCE	Drosophila melanogaster				
AUTHORS	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscophora; Ephydroidea; Drosophilidae; Drosophila.				
TITLE	1 (bases 1 to 1225)				
JOURNAL	Genoscope.				
COMMENT	Direct Submission Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaut at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.				
FEATURES	Location/Qualifiers				
source	1..1225				
	/organism="Drosophila melanogaster"				
	/plasmid="pBelobAC11"				
	/db_xref="taxon:7227"				
	/clone_lib="DrosBAC"				
	/clone="BA0161C18"				
	/note="end : SP6"				
BASE COUNT	266 a 128 c 38 g 368 t 425 others				
ORIGIN					
Query Match	13.7% ; Score 42.6; DB 12; Length 1225;				
Best Local Similarity	35.3% ; Pred. No. 17;				
Matches	78; Conservative 42; Mismatches 101; Indels 0; Gaps 0;				
QY	50	agatatagaatctgactgctgtctctctcaactaatttgataatgattgacagc	109		
DB	887	AAAAAAAAAAAAAAAAATTTTYYTAYMAAAATAAATAMWMTWTTRAAAMWMAAAAAAAAAAW	946		
QY	110	aattatgaagatctcaacgcacgcacgcagaggttgtaagtactcgtggaacatacaga	169		
DB	947	AWMTTAAAAAAWMTWMAATTAATTAATTTTATTTTAAWMTTAAWMTTAAWMTTAAATTAATTTT	1006		

OY	170	tttggctccatgcgccaataagaagaaattgcttcgaagtatttggtgatataaacacaaga	229
Db	1007	TTTTTTTTTAAAAAAMAAAAAAAAATATATTCTTTTAAATAATTTTATATATTA	1066
OY	230	ctctcctaagaagatgtaaatcttcatgatgtcttccttt	270
Db	1067	TTTTTATATTMAAAMAAATTTTWTWTWTWTWTWTWTWTWT	1107
RESULT	6		
CNS0159T			
LOCUS			
DEFINITION	CNS0159T	948 bp	DNA linear GSS 26-JUL-1999
ACCESSION	BACD13A12		of DrosBAC library from Drosophila melanogaster (fruit fly) genomic survey sequence.
VERSION	AL105179		
KEYWORDS	AL105179.1		GI:5617193
SOURCE	GSS.		
ORGANISM	fruit fly.		
	Drosophila melanogaster		
	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;		
	Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
REFERENCE	1 (bases 1 to 948)		
AUTHORS	Genoscope.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-JUL-1999) Genoscope - Centre National de Sequence BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA has been prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.		
FEATURES			
source	Location/Qualifiers		
	1..948		
	/organism="Drosophila melanogaster"		
	/plasmid="pBelobAC11"		
	/db_xref="taxon:7227"		
	/clone_1bp="drosBAC"		
	/clone="BACN13A12"		
	/note="end : 77"		
BASE COUNT	110 a 73 c 109 g 297 t	359 others	
ORIGIN			
Query Match	13.6%;	Score 42.4;	DB 12; Length 948;
Best Local Similarity	20.6%;	Fred. NO. 19;	
Matches	48; Conservative	91; Mismatches	94; Indels 0; Gaps 0;
OY	74	ctctcctaataatttatcatgatgttcacgaatatgtaagagctcaacagcag	133
Db	635	MTTMMMTHTMNMHTTTTCGKGVAGMGMTTVNGOMMMKKMKGGVGNNGMBGMM	694
OY	134	caacgagatgttgtagtctgtggaacatcacagatlttgctcatcgccstaagaga	193
Db	695	VKKGKMGKGMKCKMKMKKKKGVAKGVVMKCMKMKKKMKMKMKMKMKTKK	754
OY	194	aattgcttcagatatattgattgataaaaacaaagactctttaagagatgaaat	253
Db	755	KMTKKKKKKKKKKKAADKAKKAAAARAKAKAKAKAKAKAKKDAAWTTTTAAAT	814
OY	254	catgattgttctcttttgcttaaacataagaatgaocgfatctctttaca	306
Db	815	TWTAATTAATTTTWTWTAAATTTAAAMGTAAWMATTTAAWATTTAAWATAKATADA	867
RESULT	7		
CNS036CC			
LOCUS			
	637 bp	DNA linear	GSS 15-MAY-2000

DEFINITION	Tetradodon nigroviridis genome survey sequence PUC-Orl end of clone 215L21 of library G from Tetradodon nigroviridis, genomic survey sequence.
ACCESSION	AL229845
VERSION	AL229845.1 GI:7888840
KEYWORDS	GSS: genome survey sequence.
SOURCE	Tetradodon nigroviridis.
ORGANISM	Tetradodon nigroviridis.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphida; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetradodon.
AUTHORS	1 (bases 1 to 637) Reest-Crollius,H., Jaillon,O., Dasilva,C., Fzames,C., Fisher,C., Bouneau,L., Billault,A., Queller,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 637) Reest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fzames,C., Wincker,P., Brothier,P., Queller,F., Saurin,W. and Weissenbach,J.
AUTHORS	Human gene number estimate provided by genome wide analysis using Tetradodon nigroviridis DNA sequence
TITLE	Unpublished
JOURNAL	3 (bases 1 to 637)
REFERENCE	Genoscope.
AUTHORS	Direct Submission
TITLE	Submitted (12-APR-2000) to the EMBL/Genbank/DBJ databases
JOURNAL	This sequence is a single read and was generated as part of a large scale clone-and-sequencing project of the Tetradodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetradodon .
COMMENT	Location/Qualifiers
FEATURES	1..637
SOURCE	/organism="Tetradodon nigroviridis" /db_xref="taxon:99883" /clone="215L21" /clone_1lb="G" /note="Genoscope sequence ID : C0AG215CF11SP1-end : PUC-Orl"
BASE COUNT	180 a 95 c 80 g 224 t 58 others
ORIGIN	
Query Match	13.5%; Score 42; DB 12; Length 637;
Best Local Similarity	38.0%; Pred. No. 24;
Matches 117; Conservative 33; Mismatches 156; Indels 0; Caps 0	
QY 2	tttggttaatgcatcctttttaaatatcatatgagatgcttgccctttagatagaat 61
Db 308	TTTTTTTTTTTTTTTTTTTAAATAAAWCMMAAAWTTTTTTTTTTTMAAAAAAW 367
QY 62	atcgaatgcctcttctcaactaaatttgatcatcatgatctgaagaatgaag 121
Db 368	TTTTTTTMMTTTTTTTMMMAAAAAAATAAAWTTTTTCCCAATTTTWTW 427
QY 122	tctaacgcacagacgcaggttgtaagtaactgtggacaatcacaagatttggctcat 181
Db 428	WATRAAAAAAATAAAWTTTTTTTMAAAAAAATAAAWMAAAAAWMTTMAAAAA 487
QY 182	gccctaaagaagaatgagcttcagatatttggaattaaacaagaagcttcttaag 241
Db 488	AMTTTTTTTTTAAAAAATAAAWTTTTTTTTTMAAAAAAATAAAWTTTTTMAA 547
QY 242	atgtaaaatttcatgatgttctcttttgcgtaaacacaagaatgaacgcatctt 301
Db 548	AMAAAAATTTTTTTTTTTTMMTMMTTTTTTATTTTTTAAAAAATAAAATTTT 607
QY 302	ttacattt 309
Db 608	TTWTWT 615

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RESULT      8
CNS00H87    1101 bp  DNA      linear  GSS 03-JUN-1999
LOCUS
DEFINITION   Drosophila melanogaster genome survey sequence TE3 end of BAC:
BAC34J09 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION    AL073055.1  GI:4952936
VERSION
KEYWORDS
SOURCE
ORGANISM     Drosophila melanogaster
              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
              Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
              Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE    Genoscope.
              Direct Submission
              Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
              BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
              Web : www.genoscope.cns.fr)
              Determination of this BAC-end sequence was carried out as part of a
              collaboration with the Berkeley Drosophila Genome Project (BDGP).
              The BDGP is constructing a physical map of the Drosophila
              melanogaster genome using these BACs. For further information
              please see http://www.fruitfly.org The BDGP Drosophila
              melanogaster BAC library was prepared by Kazutoyo Osogawa and
              Aaron Mammoser in Pieter de Jong's laboratory in the Department of
              Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
              NY. The library is named RPCI-98 and was constructed by partial
              EcoRI digestion of Drosophila DNA provided by the BDGP from the
              isogenic strain y2; cn bw sp, the same strain used for the BDGP's
              p1 and EST libraries. A more detailed description of the library
              and how to order individual BAC clones, the entire library, or
              filters for hybridization from the BACPAC Resource Center can be
              found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
  source
    1..1101
    /organism="Drosophila melanogaster"
    /db_xref="taxon:7227"
    /clone_lib="RPCI-98"
    /clone="BACR34J09"
    /note="end : TER3"
BASE COUNT    149 a      86 c      62 g      380 t      424 others
ORIGIN
Query Match      13.3%; Score 41.6; DB 12; Length 1101;
Best Local Similarity 34.8%; Pred. No. 28;
Matches 104; Conservative 1; Mismatches 194; Indels 0; Gaps 0;
QY  2 ttgtttaacatcctttttaaatatcatgagtgatgcttcgctttagatagaat 61
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  91 TTTTNTTTTTTTTTTTTTTTTTTTTTTTTTTTTNTTNTTNTTNTTNTTNTTNTN 150
QY  62 atcgatgcgctctctcctaatttgatcatgattgacagcaatatgaag 121
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  151 ATCTTAATTAATCTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNT 210
QY  122 tctaacgcacgcagcaggttgtaagtaactgtagaacatcacagattgctccat 181
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  211 NNANNNNNNNNNNTTATTTTTTTTTTTTTTTTNTNNGNNNTTATTTTATATNT 270
QY  182 gccctaaagaaattgcttccagattctgattaaacaagaacttccttaag 241
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  271 AANNNNNNNNNAATAATTTNANNANANNAANNAATAATNTTNTTTTATATANN 330
QY  242 atgtaaaattctatgatttcttcttgcataaaactaagaatgaagcgatctc 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  331 ANNNNNNAANNNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTTNTT 389

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RESULT      9
BI314726/c  402 bp  mRNA      linear  EST 20-JUL-2001
LOCUS
DEFINITION   dae53f11.y1 Blackshear/Soares normalized Xenopus egg library
Xenopus laevis cDNA clone IMAGE:4678028 5', mRNA sequence.
ACCESSION    BI314726
VERSION
KEYWORDS
SOURCE
ORGANISM     African clawed frog.
              Xenopus laevis
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
              Xenopodinae; Xenopus.
              1 (bases 1 to 402)
REFERENCE    Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Page,D.,
              Martin,J., Wylie,T., Underwood,K., Treising,B., Bowers,Y., Person
              'B.', Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
              Waterston,R. and Wilson,R.
              Washu Xenopus EST project, 1999
              Unpublished (1999)
              Contact: Sandy Clifton, Ph.D.
              Washington University School of Medicine
              4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
              Tel: 314 286 1800
              Fax: 314 286 1810
              Email: est@wustl.edu
              Library constructed by Bento Soares and M. Fatima Bonaldo
              (University of Iowa). DNA Sequencing by: Washington University
              Genome Sequencing Center
              Clone distribution: Xenopus clones from this library are available
              through the I.M.A.G.E. Consortium/LINL at: info@image.llnl.gov
              Seq primer: -40RP from GIPCO
              High quality sequence stop: 371.
FEATURES
  source
    1..402
    /organism="Xenopus laevis"
    /db_xref="taxon:8355"
    /clone="IMAGE:4678028"
    /clone_lib="Blackshear/Soares normalized Xenopus egg
    library"
    /sex="female"
    /tissue_type="unfertilized egg"
    /cell_type="unfertilized egg"
    /dev_stage="unfertilized egg"
    /lab_host="DH10B"
    /note="Vector: pT7T3-Pac; Site.1: EcoRI; Site.2: NotI.
    PolyA-selected mRNA was prepared from unfertilized Xenopus
    laevis eggs. The library was constructed in the vector
    pT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and
    Soares, M.B. 'Normalization and subtraction: two
    approaches to facilitate gene discovery', Genome Research
    6:791-806, 1996. The first strand synthesis used a
    NotI-drl8 primer; double stranded cDNAs were ligated to
    EcoRI adapters, digested with NotI, and directionally
    cloned into the NotI and EcoRI-digested pT7T3-Pac vector.
    The library contained approximately 7.2 x 105
    recombinants, with average insert sizes of 1-1.5 kb."
BASE COUNT    137 a      49 c      46 g      170 t
ORIGIN
Query Match      13.1%; Score 41; DB 10; Length 402;
Best Local Similarity 47.8%; Pred. No. 42;
Matches 119; Conservative 0; Mismatches 130; Indels 0; Gaps 0;
QY  14 tccctttaaacatcagtgatgcttgcctttagatataagaatcctgagtcgt 73
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  393 TCATTTTAAATGCTATATATATATATATATATATATATATATATATATATAT 334
QY  74 ctctctactaaatttgattcatgatgtgacgacatattgaagagtcctaacgcag 133
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db  333 ATATATATATATATATATATATATATATATATATATATATATATATATAT 274

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OY	258	atgcttcttttgcttaaaccaagaatttaacgtatcttcaca	306
		: : : :	
Db	663	AMATTTHATATAKAAGCTTAAAGAANMADNATACGAGAATTTMAA	615
RESULT	11	CNS010Y8	810 bp DNA linear GSS 26-JUL-1991
LOCUS	CNS010Y8/c		
DEFINITION		Drosophila melanogaster genome survey sequence sp6 end of BAC BACN05D22 of DrosBAC library from Drosophila melanogaster (fruit fly) genomic survey sequence.	
ACCESSION		AL099578	
VERSION		AL099578.1	GI:5611189
KEYWORDS		GSS.	
SOURCE		fruit fly.	
ORGANISM		Drosophila melanogaster	
		Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.	
REFERENCE		Genoscope. Direct Submission Submitted (23-Jul-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)	
AUTHORS		Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.	
FEATURES		Location/Qualifiers	
source		1..810	
		/organism="Drosophila melanogaster"	
		/plasmid="pBelobAC11"	
		/db_xref="taxon:7227"	
		/clone_1lb="DrosBAC"	
		/clone="BACN05D22"	
		/note="end : SP6"	
BASE COUNT		247 a 138 c 168 g 170 t	87 others
ORIGIN			
		Query Match	13.1%; Score 40.8; DB 12; Length 810;
		Best local Similarity	52.0% Pred. No. 43;
		Matches	51; Conservative 12; Mismatches 35; Indels 0; Gaps 0;
OY	177	tccatgccctaagagaatggccttcagatatcttgagttaaacaagaacttcct	236
		: :	
Db	108	TCCATTGCCCTTCGTGAATATGGCCTTCACCKHWTYACCATHAMADGCANAGCGGTTGCG	49
OY	237	aagagatgtaaaatttcgatgctgccttccttccttccttcgt	274
Db	48	ANGANAANGAANTTTATNTATNTTTTCTTTTAKMT	11
RESULT	12	AZ674355	940 bp DNA linear GSS 14-DEC-2000
LOCUS	AZ674355		
DEFINITION		ENT16.64R Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, DNA sequence.	
ACCESSION		AZ674355	
VERSION		AZ674355.1	GI:11811501
KEYWORDS		GSS.	
SOURCE		Entamoeba histolytica.	
ORGANISM		Entamoeba histolytica	
		Eukaryota; Entameobidae; Entamoeba.	
REFERENCE		1 (bases 1 to 940) Loftus,B., Van Aken,S. and Fraser,C. Determination of clone and sequences from Entamoeba histolytica	
AUTHORS			
TITLE			

RESULT	14
CNS014PQ/c	
LOCUS	CNS014PQ
DEFINITION	Drosophila melanogaster genome survey sequence SP6 end of BAC BACN1P22 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION	AL104456
VERSION	ALI04456.1 GI:5616067
KEYWORDS	GSS,
SOURCE	fruit fly.
ORGANISM	Drosophila melanogaster
REFERENCE	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 987)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr Web : www.genoscope.cns.fr)
COMMENT	determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CPHF (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeltoBAC11.

[illegible]

RESULT 15		
CNS01U90	LOCUS	DEFINITION
CNS01U90	524 bp	DNA linear GSS 12-MAY-2000
Tetradon nigroviridis genome survey sequence pUC-ori end of clone 196C24 of library G from Tetradon nigroviridis, genomic survey sequence.		

ACCESSION	AL167541
VERSION	AL167541.1
KEYWORDS	GSS; genome survey sequence.
ORGANISM	Tetraodon nigroviridis.
TITLE	Tetraodon nigroviridis
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neuteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neuteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
REFERENCE	1 (bases 1 to 524)
AUTHORS	Roest-Collins,H., Jallion,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 524)
AUTHORS	Roest-Collins,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 524)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (12-APR-2000) to the EMBL/GenBank/DBD databases
COMMENT	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetraodon .

FEATURES	source	Location/Qualifiers
	1. .524	/organism="Heterodon nigriviridis"
		/db_xref="taxon:99883"
		/clone="196C24"
		/clone_1lb="G"
		/note="Genoscope sequence ID : COAG156BB12SPl-end
		PUC-01"
BASE COUNT	124 a	15 c 24 g 298 t 63 others
BRIGIN		

	Query Match:	12.9%	Score 40.4;	DB 12;	Length 524;
	Best Local Similarity	42.1%;	Pred. No. 55;		
	Matches 59;	Conservative 25;	Mismatches 56;	Indels 0;	Gaps 0;
Oy	148	agacgtctggagacatcacagatttgcctccaccctaagaagaattgcttcaga	207		
Dd	53	AGTAAAGACGCGACGAMACCAGTATTTTKTKTTTTWDWTTWWAAAAAASMMMMMMMMMMW	112		
Oy	208	ttaattggaattaaacaagaacttcctaagaagtataaatcttcacgatgtttcctt	267		
	: :				

Db 113 WWWWWWWWWWWWWWWWWWWWWTTTTTTTTTATWTTATTTTTTTTTTTW 172
Qy 268 ttTgCtaactaaagaat 287
||| |||| || ||
Db 173 TTTTTTAAATATAATAT 192

Search completed: September 9, 2002, 20:42:51
Job time: 15649 sec

